

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/593,119  
Source: FWP  
Date Processed by STIC: 9/28/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/593,119

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2        Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3        Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
  
- 4        Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5        Variable Length     Sequence(s)        contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6        PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7        Skipped Sequences  
    (OLD RULES)     Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8        Skipped Sequences  
    (NEW RULES)     Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
  
- 9        Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10        Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
  
- 11        Use of <220>     Sequence(s)        missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."  
                          Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
  
- 12        PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13        Misuse of n/Xaa     "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

## RAW SEQUENCE LISTING

DATE: 09/28/2006

PATENT APPLICATION: US/10/593,119

TIME: 10:37:04

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\09282006\J593119.raw

4 <110> APPLICANT: Degussa AG  
 6 <120> TITLE OF INVENTION: Novel alcohol dehydrogenases  
 8 <130> FILE REFERENCE: S-IPM-PAT/Dr. Re-ko - K1419 EP  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/593,119  
 C--> 10 <141> CURRENT FILING DATE: 2006-09-18  
 10 <160> NUMBER OF SEQ ID NOS: 68  
 12 <170> SOFTWARE: PatentIn version 3.1

*see item 4 on  
 Enr summary sheet*

**Does Not Comply  
 Corrected Diskette Needed**

## ERRORED SEQUENCES

2654 <210> SEQ ID NO: 68  
 2656 <211> LENGTH: 1047  
 2658 <212> TYPE: DNA  
 2660 <213> ORGANISM: unknown  
 2662 <220> FEATURE:  
 2664 <221> NAME/KEY: source  
 2665 <223> OTHER INFORMATION: ZF0050310= Arthrobacter paraffineus  
 2667 <400> SEQUENCE: 68  
 2668 atgaaggcaa tccagtacac gagaatcggc gcagaacccg aactcacgga gattcccaaaa 60  
 2670 cccgagcccc gtccagggtga agtgctcctg gaagtcaccg ctgccggcgt ctgccactcg 120  
 2672 gacgacttca tcatgagcct gcccgaagag cagtacacct acggccttcc tctcacgctc 180  
 2674 ggccacgaag gcgccggccg ggtcgccgcc gtcggcgagg gcgtcgaagg actcgacatc 240  
 2676 ggaaccaatg tcgtcgtcta cggaccctgg ggctgtggca gctgttggca ctgctcgcaa 300  
 2678 ggactcgaaa actactgttc tcggggcaaaa gaactcggca tcaatcctcc tgggtctcgg 360  
 2680 gcacccggcg cgttggccga attcatgac gtcgattcac ctgccacct cgtcccgatc 420  
 2682 ggcgacctcg atccgggtcaa gacggtgcca ctgaccgacg ccggtctgac tccgtatcac 480  
 2684 gcgatcaagc gttcactgcc gaaacttcgc ggtggcgcg acgccgtcgt catcggtacc 540  
 2685 ggcgggtctcg gccatgtcgc catccaactc ctccgccacc tctcggcagc aaccgtcatc 600  
 2687 gcactcgacg tgagcgcgga caagctcgaa ctggcaacca aggtaggcgc tcacgaagtg 660  
 2689 gtcctgtccg acaaggacgc ggccgagAAC gtccgcagga tcaccggaag tcagggcgcc 720  
 2691 gcactggttc tcgacttcgt cggctatcag cccaccatcg acaccgcgat ggctgtcgcc 780  
 2693 ggcgtcggat cggacgtcac gatcgtcggg atcggcgacg ggcaggccca tgccaaagtc 840  
 2695 gggttcttcc aaagtcctta cgaggcttct gtgacagttc cgtactgggg tgcccgaac 900  
 2697 gagctgatcg aattgatcga cctggcgcac gccggcatct tcgacatcgc ggtggagacc 960  
 2699 ttcagtctcg acaacggcgc cgaagcgat cgaacgactgg ccgccggaac gtcacgaggc 1020  
 E--> 2701 cgcgcgggtg tgggtccctg tctgtag 1047 ← insert

*see pp 2, 5*

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/593,119

DATE: 09/28/2006  
TIME: 10:37:05

Input Set : A:\PTO.RJ.txt  
Output Set: N:\CRF4\09282006\J593119.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 26,27,33  
Seq#:2; Line(s) 97,98,104  
Seq#:6; Line(s) 323  
Seq#:7; Line(s) 374  
Seq#:8; Line(s) 425  
Seq#:9; Line(s) 476  
Seq#:10; Line(s) 527  
Seq#:11; Line(s) 578  
Seq#:14; Line(s) 707  
Seq#:15; Line(s) 760  
Seq#:16; Line(s) 817  
Seq#:17; Line(s) 881  
Seq#:35; Line(s) 1670,1671,1677  
Seq#:36; Line(s) 1714,1715,1721  
Seq#:40; Line(s) 1857  
Seq#:41; Line(s) 1894  
Seq#:42; Line(s) 1929  
Seq#:43; Line(s) 1966  
Seq#:44; Line(s) 2002  
Seq#:45; Line(s) 2039  
Seq#:50; Line(s) 2197  
Seq#:51; Line(s) 2238

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/593,119

DATE: 09/28/2006

TIME: 10:37:05

Input Set : A:\PTO.RJ.txt

Output Set : N:\CRF4\09282006\J593119.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:29 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:30 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:31 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:32 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:33 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:34 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:35 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:36 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:100 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:101 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:102 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:103 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:104 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:105 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:106 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:107 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:277 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:278 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:279 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:280 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:281 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:282 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:283 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:321 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:322 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:323 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:324 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:325 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:326 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:327 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:328 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:329 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:372 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:373 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:374 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:375 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:376 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:377 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:378 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:379 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:380 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:423 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:424 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:425 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:426 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:427 M:259 W: Allowed number of lines exceeded, <223> Other Information:

## VERIFICATION SUMMARY

DATE: 09/28/2006

PATENT APPLICATION: US/10/593,119

TIME: 10:37:05

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\09282006\J593119.raw

L:428 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:429 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:430 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:431 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1562 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1725 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2701 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1047 SEQ:68

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5

&lt;210&gt; 1

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; unknown

&lt;220&gt;

&lt;221&gt; source

<223> ZF0002326= Actinoplanes missouriensis; ZF0003505= Streptomyces;  
 ZF0050197= Pseudomonas oleovorans; ZF0050294= Rhodococcus; ZF0050330= Bacillus;  
 ZF0051303= Bacterium; ZF0051337= Methylobacter; ZF0051321= Bacterium; ZF0050782=  
 Lactobacillus bulgaricus; ZF0050544= Phyllobacterium rubiacearum; ZF0002852=  
 Rhodococcus; ZF0050310= Arthrobacter paraffineus; ZF0002862= Streptomyces  
 clavuligerus; ZF0050292= Bacterium; ZF0002031= Streptomyces; ZF0002349=  
 Streptomyces spectabilis; ZF0002434= Streptomyces; ZF0002437= Streptomyces;  
 ZF0003712= Micromonospora; ZF0003765= Streptomyces; ZF0051305= Bacterium;  
 ZF0003513= Actinomyces; ZF0050993= Kocuria; ZF0002018= Streptomyces; ZF0003767=  
 Actinomyces; ZF0002332= Streptomyces diastatochromogenes; ZF0003768=  
 Actinomyces; ZF0002379= Streptomyces coelestis; ZF0002351= Nonomuraea  
 roseoviolacea; ZF0003769= Actinomyces;

&lt;400&gt; 1

Per 1.823 of Sequence Rules, <223> response  
 has a MAXIMUM of 4 lines. Please insert a <220>  
 above every 5<sup>th</sup> line, and a <223> at beginning of every  
 5<sup>th</sup> line

<220> <223> Rhodococcus; ZF0050310= Arthrobacter paraffineus; ZF0002862= Streptomyces  
 clavuligerus; ZF0050292= Bacterium; ZF0002031= Streptomyces; ZF0002349=  
 Streptomyces spectabilis; ZF0002434= Streptomyces; ZF0002437= Streptomyces;  
 ZF0003712= Micromonospora; ZF0003765= Streptomyces; ZF0051305= Bacterium;  
 ZF0003513= Actinomyces; ZF0050993= Kocuria; ZF0002018= Streptomyces; ZF0003767=  
 Actinomyces; ZF0002332= Streptomyces diastatochromogenes; ZF0003768=  
 Actinomyces; ZF0002379= Streptomyces coelestis; ZF0002351= Nonomuraea  
 roseoviolacea; ZF0003769= Actinomyces;

The above is a sample of global errors.